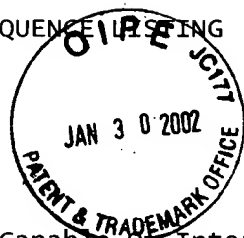


SEQUENCE LISTING

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TECH CENTER 1600/2900



<110> Aventis Pharma, S.A.

<120> Polyopeptide (MBP1) Capable of Interacting with Oncogenic Mutants of The P53 Protein

<130> ST98033

<140> 09/829,936

<141> 2001-04-11

<150> FR9812754

<151> 1998-10-12

<160> 33

<170> PatentIn version 3.1

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<213> Artificial Sequence

<220>

<223> Oligonucleotide

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23

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<211> 29

<212> DNA

<213> Artificial Sequence

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<223> Oligonucleotide 3' -393 (p53)

<400> 2

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29

<210> 3

<211> 15

<212> DNA

<213> Artificial Sequence

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<223> oligonucleotide H175 3'

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<210> 4

<211> 15

<212> DNA

<213> Artificial Sequence

<220>

<223> oligonucleotide W248 3'

<400> 4

gggcctccag ttcac

15

<210> 5

<211> 15

<212> DNA

<213> Artificial Sequence

<220>

<223> oligonucleotide H273 3'

<400> 5

acaaacatgc acctc

15

<210> 6

<211> 15

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<213> Artificial Sequence

<220>
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15

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<211> 23

<212> DNA

<213> Artificial Sequence

<220>
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23

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<211> 1021

<212> DNA

<213> Artificial Sequence

<220>
<223> Fragment C-term MBP1 murine: CDS (1)...(885)

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gagccaggct tccagttggg acctaacaac cgctcttgtg tggatgtgaa tgagtgtgac 180
atgggagccc catgtgagca gcgctgcttc aactcctatg ggaccttcct gtgtcgctgt 240
aaccagggtc atgagctgca ccgggatggc ttctcctgca gcgatatcga tgagtgcggc 300
tactccagtt acctctgcca gtaccgctgt gtcaacgagc caggccgatt ctctgtcac 360
tgcccacaag gctaccagct gctggctaca aggctctgcc aagatattga cgagtgtgaa 420
acagggtgcac accaatgttc tgaggcccaa acctgtgtca acttccatgg gggttaccgc 480
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aagggccatg tgggggcccc ttccccctcc catagcttaa gcagccccgg gggcctaggg 960
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<210> 9

<211> 295

<212> PRT

<213> Artificial Sequence

<220>

<223> Fragment C-term MBP1 murine

<400> 9

Cys Thr Cys Pro Asp Gly Tyr Arg Lys Ile Gly Pro Glu Cys Val Asp
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Ile Asp Glu Cys Arg Tyr Arg Tyr Cys Gln His Arg Cys Val Asn Leu
20 25 30

Pro Gly Ser Phe Arg Cys Gln Cys Glu Pro Gly Phe Gln Leu Gly Pro
35 40 45

Asn Asn Arg Ser Cys Val Asp Val Asn Glu Cys Asp Met Gly Ala Pro
50 55 60

Cys Glu Gln Arg Cys Phe Asn Ser Tyr Gly Thr Phe Leu Cys Arg Cys
65 70 75 80

Asn Gln Gly Tyr Glu Leu His Arg Asp Gly Phe Ser Cys Ser Asp Ile
85 90 95

Asp Glu Cys Gly Tyr Ser Ser Tyr Leu Cys Gln Tyr Arg Cys Val Asn
100 105 110

Glu Pro Gly Arg Phe Ser Cys His Cys Pro Gln Gly Tyr Gln Leu Leu
115 120 125

Ala Thr Arg Leu Cys Gln Asp Ile Asp Glu Cys Glu Thr Gly Ala His
130 135 140

Gln Cys Ser Glu Ala Gln Thr Cys Val Asn Phe His Gly Gly Tyr Arg
145 150 155 160

Cys Val Asp Thr Asn Arg Cys Val Glu Pro Tyr Val Gln Val Ser Asp
 165 170 175
 Asn Arg Cys Leu Cys Pro Ala Ser Asn Pro Leu Cys Arg Glu Gln Pro
 180 185 190
 Ser Ser Ile Val His Arg Tyr Met Ser Ile Thr Ser Glu Arg Ser Val
 195 200 205
 Pro Ala Asp Val Phe Gln Ile Gln Ala Thr Ser Val Tyr Pro Gly Ala
 210 215 220
 Tyr Asn Ala Phe Gln Ile Arg Ser Gly Asn Thr Gln Gly Asp Phe Tyr
 225 230 235 240
 Ile Arg Gln Ile Asn Asn Val Ser Ala Met Leu Val Leu Ala Arg Pro
 245 250 255
 Val Thr Gly Pro Arg Glu Tyr Val Leu Asp Leu Glu Met Val Thr Met
 260 265 270
 Asn Ser Leu Met Ser Tyr Arg Ala Ser Ser Val Leu Arg Leu Thr Val
 275 280 285
 Phe Val Gly Ala Tyr Thr Phe
 290 295

<210> 10
 <211> 39
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> oligonucleotide c-myc 5'

<400> 10
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39

<210> 11
 <211> 39
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> oligonucleotide c-myc 3'

<400> 11
gatctcaggt cctcctcgga gatcagcttc tgctccatg 39

<210> 12

<211> 45

<212> DNA

<213> Artificial Sequence

<220>

<223> MCS 5'

<400> 12
gatctcggtc gacctgcatg caattcccgg gtgcggccgc gagct 45

<210> 13

<211> 37

<212> DNA

<213> Artificial Sequence

<220>

<223> MCS 3'

<400> 13
cgcgccgca cccgggaatt gcatgcaggt cgaccga 37

<210> 14

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> oligonucleotide 3' mMBP1

<400> 14
cggctactggc agaggtaact gg 22

<210> 15

<211> 1513

<212> DNA

<213> Artificial Sequence

<220>

<223> MBP1 murine (complete sequence): CDS (49)...(1377)

<400> 15

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gcgtccccac aggatcccga ggagccggac agctacacgg aatgcacaga tggctatgag    180
tgggatgcag acagccagca ctgccgggat gtcaacgagt gcctgaccat cccggaggct    240
tgcaagggtg agatgaaatg catcaaccac tacggggggtt atttgtgtct gcctcgctct    300
gctgccgtca tcagtgatct ccatggtgaa ggacctccac cgccagcggc ccatgctcaa    360
caaccaaacc cttgcccgcg gggctacgag cctgatgaac aggagagctg tgtggatgtg    420
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aatgagtgtg acatgggagc cccatgtgag cagcgtgct tcaactccta tgggaccttc    720
ctgtgtcgct gtaaccaggg ctatgagctg caccgggatg gcttctcctg cagcgatatc    780
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ttctcctgtc actgccaca aggctaccag ctgctggcta caaggctctg ccaagatatt    900
gacgagtgtg aaacaggtgc acaccaatgt tctgaggccc aaacctgtgt caacttccat    960
gggggttacc gctgtgtgga caccaaccgt tgtgtggagc cctatgtcca agtgtcagac   1020
aaccgctgcc tctgccctgc ctccaatccc ctttgtcgag agcagccttc atccattgtg   1080
caccgctaca tgagcatcac ctgagagcga agtgtgcctg ctgacgtgtt tcagatccag   1140
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agctaccggg ccagctctgt actgagactc acggtctttg tgggagccta taccttctga   1380
agaccctcag ggaagggccca tgtgggggcc ccttccccct cccatagctt aagcagcccc   1440
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gaaagaagga aaa                                     1513
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<210> 16

<211> 442

<212> PRT

<213> Artificial Sequence

<220>

<223> MBP1 murine (complete sequence)

<400> 16

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Phe Leu Leu Leu Leu Leu Gly Ala Ala Ser Pro Gln Asp Pro Glu Glu
20 25 30

Pro Asp Ser Tyr Thr Glu Cys Thr Asp Gly Tyr Glu Trp Asp Ala Asp
35 40 45

Ser Gln His Cys Arg Asp Tyr Asn Glu Cys Leu Thr Ile Pro Glu Ala
50 55 60

Cys Lys Gly Glu Met Lys Cys Ile Asn His Tyr Gly Gly Tyr Leu Cys
65 70 75 80

Leu Pro Arg Ser Ala Ala Val Ile Ser Asp Leu His Gly Glu Gly Pro
85 90 95

Pro Pro Pro Ala Ala His Ala Gln Gln Pro Asn Pro Cys Pro Gln Gly
100 105 110

Tyr Glu Pro Asp Glu Gln Glu Ser Cys Val Asp Val Asp Glu Cys Thr
115 120 125

Gln Ala Leu His Asp Cys Arg Pro Ser Gln Asp Cys His Asn Leu Pro
130 135 140

Gly Ser Tyr Gln Cys Thr Cys Pro Asp Gly Tyr Arg Lys Ile Gly Pro
145 150 155 160

Glu Cys Val Asp Ile Asp Glu Cys Arg Tyr Arg Tyr Cys Gln His Arg
165 170 175

Cys Val Asn Leu Pro Gly Ser Phe Arg Cys Gln Cys Glu Pro Gly Phe
180 185 190

Gln Leu Gly Pro Asn Asn Arg Ser Cys Val Asp Val Asn Glu Cys Asp
195 200 205

Met Gly Ala Pro Cys Glu Gln Arg Cys Phe Asn Ser Tyr Gly Thr Phe
210 215 220

Leu Cys Arg Cys Asn Gln Gly Tyr Glu Leu His Arg Asp Gly Phe Ser
225 230 235 240

Cys Ser Asp Asp Glu Cys Gly Tyr Ser Ser Tyr Leu Cys Gln Tyr Arg
245 250 255

Cys Val Asn Glu Pro Gly Arg Phe Ser Cys His Cys Pro Gln Gly Tyr
260 265 270

Gln Leu Leu Ala Thr Arg Leu Cys Gln Asp Ile Asp Glu Cys Glu Thr
275 280 285

Gly Ala His Gln Cys Ser Glu Ala Gln Thr Cys Val Asn Phe His Gly
290 295 300

Gly Tyr Arg Cys Val Asp Thr Asn Arg Cys Val Glu Pro Tyr Val Gln
305 310 315 320

Val Ser Asp Asn Arg Cys Leu Cys Pro Ala Ser Asn Pro Leu Cys Arg
325 330 335

Glu Gln Pro Ser Ser Ile Val His Arg Tyr Met Ser Ile Thr Ser Glu
340 345 350

Arg Ser Val Pro Ala Asp Val Phe Gln Ile Gln Ala Thr Ser Val Tyr
355 360 365

Pro Gly Ala Tyr Asn Ala Phe Gln Ile Arg Ser Gly Asn Thr Gln Gly
370 375 380

Asp Phe Tyr Ile Arg Gln Ile Asn Asn Val Ser Ala Met Leu Val Leu
385 390 395 400

Ala Arg Pro Val Thr Gly Pro Arg Glu Tyr Val Leu Asp Leu Glu Met
405 410 415

Val Thr Met Asn Ser Leu Met Ser Tyr Arg Ala Ser Ser Val Leu Arg
420 425 430

Leu Thr Val Phe Val Gly Ala Tyr Thr Phe
435 440

<210> 17

<211> 21

<212> DNA

<213> Artificial Sequence

<220>
<223> oligonucleotide 3' hMBP1

<400> 17
ctccgctccg aggtgatggt c 21

<210> 18

<211> 21

<212> DNA

<213> Artificial Sequence

<220>
<223> oligonucleotide 5' hMBP1

<400> 18
tgtagctact ccagctacct c 21

<210> 19

<211> 1122

<212> DNA

<213> Artificial Sequence

<220>
<223> Human cDNA MBP1

<400> 19
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cttgggatca gcttctcctc aggattctga agagcccgac agctacacgg aatgcacaga 180
tggctatgag tgggaccag acagccagca ctgccgggat gtcaacgagt gtctgaccat 240
ccctgaggcc tgcaaggggg aaatgaagtg catcaaccac tacgggggct acttgtgcct 300
gccccgctcc gctgccgtca tcaacgacct acacggcgag ggacccccgc caccagtgcc 360
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tgtggatgtg gacgagtgtg cccaggccct gcacgactgt cggcccagcc aggactgcca 480
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tgttgatgtg aacgagtgtg acatgggggc cccatgagag cagcgctgct tcaactccta 720

tgggaccttc ctgtgtcgct gccaccaggg ctatgagctg catcgggatg gcttctcctg	780
cagtgatatt gatgagtgtg gctactccag ctacctctgt cagtaccgct gcgtcaacga	840
gccaggccgt ttctcctgcc actgcccaca gggttaccag ctgctggcca cacgcctctg	900
ccaagacatt gatgagtgtg agtctggtgc gcaccagtgc tccgaggccc aaacctgtgt	960
caacttccat gggggctacc gctgctgga caccaaccgc tgcgtggagc cctacatcca	1020
ggtctctgag aaccgctgtc tctgcccggc ctccaaccct ctatgtcgag agcagccttc	1080
atccattgtg caccgctaca tgaccatcac ctcggagcgg ag	1122

<210> 20

<211> 684

<212> DNA

<213> Artificial Sequence

<220>

<223> Human cDNA MBP1 (partial sequence)

<400> 20

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tgtgagtctg gtgcgacca gtgctccgag gcccaaacct gtgtcaactt ccatgggggc	180
taccgctgcg tggacaccaa ccgctgctg gagccctaca tccaggtctc tgagaaccgc	240
tgtctctgcc cggcctcaa ccctctatgt cgagagcagc cttcatccat tgtgcaccgc	300
tacatgacca tcacctgga gcggagcgtg cccgctgacg tgttccagat ccaggcgacc	360
tccgtctacc ccggtgccta caatgccttt cagatccgtg ctggaaactc gcagggggac	420
ttttacatta ggcaaatcaa caacgtcagc gccatgctgg tcctcgcccg gccggtgacg	480
ggcccccggt agtacgtgct ggacctggag atggtcacca tgaattccct catgagctac	540
cgggccagct ctgtactgag gctcaccgtc tttgtagggg cctacacctt ctgaggagca	600
ggaggagacc accctccctg cagctaccct agctgaggag cctgttgtga ggggcagaat	660
gagaaaggca ataaaggag aaag	684

<210> 21

<211> 1422

<212> DNA

<213> Artificial Sequence

<220>

<223> Human MBP1 (complete sequence): CDS (59)...(1387)

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gatggctatg agtgggaccc agacagccag cactgccggg atgtcaacga gtgtctgacc 180
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cataacttgc ctggctccta tcagtgcacc tgccctgatg gttaccgcaa gatcggggcc 480
gagtgtgtgg acatagacga gtgccgctac cgctactgcc agcaccgctg cgtgaacctg 540
cctggctcct tccgctgccg gtgcgagccg ggcttccagc tggggcctaa caaccgctcc 600
tgtgttgatg tgaacgagtg tgacatgggg gccccatgcg agcagcgctg cttcaactcc 660
tatgggacct tcctgtgtcg ctgccaccag ggctatgagc tgcatacggg tggcttctcc 720
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tgttgtgagg ggcagaatga gaaaggcaat aaaggagaaa ag 1422

<210> 22

<211> 443

<212> PRT

<213> Artificial Sequence

<220>

<223> Human MBP1 (complete sequence)

<400> 22

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 20 25 30
 Pro Asp Ser Tyr Thr Glu Cys Thr Asp Gly Tyr Glu Trp Asp Pro Asp
 35 40 45
 Ser Gln His Cys Arg Asp Val Asn Glu Cys Leu Thr Ile Pro Glu Ala
 50 55 60
 Cys Lys Gly Glu Met Lys Cys Ile Asn His Tyr Gly Gly Tyr Leu Cys
 65 70 75 80
 Leu Pro Arg Ser Ala Ala Val Ile Asn Asp Leu His Gly Glu Gly Pro
 85 90 95
 Pro Pro Pro Val Pro Pro Ala Gln His Pro Asn Pro Cys Pro Pro Gly
 100 105 110
 Tyr Glu Pro Asp Asp Gln Asp Ser Cys Val Asp Val Asp Glu Cys Ala
 115 120 125
 Gln Ala Leu His Asp Cys Arg Pro Ser Gln Asp Cys His Asn Leu Pro
 130 135 140
 Gly Ser Tyr Gln Cys Thr Cys Pro Asp Gly Tyr Arg Lys Ile Gly Pro
 145 150 155 160
 Glu Cys Val Asp Ile Asp Glu Cys Arg Tyr Arg Tyr Cys Gln His Arg
 165 170 175
 Cys Val Asn Leu Pro Gly Ser Phe Arg Cys Gln Cys Glu Pro Gly Phe
 180 185 190
 Gln Leu Gly Pro Asn Asn Arg Ser Cys Val Asp Val Asn Glu Cys Asp
 195 200 205
 Met Gly Ala Pro Cys Glu Gln Arg Cys Phe Asn Ser Tyr Gly Thr Phe
 210 215 220
 Leu Cys Arg Cys His Gln Gly Tyr Glu Leu His Arg Asp Gly Phe Ser
 225 230 235 240
 Cys Ser Asp Ile Asp Glu Cys Ser Tyr Ser Ser Tyr Leu Cys Gln Tyr
 245 250 255

Arg Cys Val Asn Glu Pro Gly Arg Phe Ser Cys His Cys Pro Gln Gly
260 265 270

Tyr Gln Leu Leu Ala Thr Arg Leu Cys Gln Asp Ile Asp Glu Cys Glu
275 280 285

Ser Gly Ala His Gln Cys Ser Glu Ala Gln Thr Cys Val Asn Phe His
290 295 300

Gly Gly Tyr Arg Cys Val Asp Thr Asn Arg Cys Val Glu Pro Tyr Ile
305 310 315 320

Gln Val Ser Glu Asn Arg Cys Leu Cys Pro Ala Ser Asn Pro Leu Cys
325 330 335

Arg Glu Gln Pro Ser Ser Ile Val His Arg Tyr Met Thr Ile Thr Ser
340 345 350

Glu Arg Ser Val Pro Ala Asp Val Phe Gln Ile Gln Ala Thr Ser Val
355 360 365

Tyr Pro Gly Ala Tyr Asn Ala Phe Gln Ile Arg Ala Gly Asn Ser Gln
370 375 380

Gly Asp Phe Tyr Ile Arg Gln Ile Asn Asn Val Phe Ala Met Leu Val
385 390 395 400

Leu Ala Arg Pro Val Thr Gly Pro Arg Glu Tyr Val Leu Asp Leu Glu
405 410 415

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420 425 430

Arg Leu Thr Val Phe Val Gly Ala Tyr Thr Phe
435 440

<210> 23

<211> 817

<212> DNA

<213> Artificial Sequence

<220>

<223> cDNA MBP1 murine (partial sequence)

<400> 23

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gcgtccccac aggatcccga ggagccggac agctacacgg aatgcacaga tggctatgag	180
tgggatgcag acagccagca ctgccgggat gtcaacgagt gcctgaccat cccggaggct	240
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ctgtgtcgct gtaaccaggg ctatgagctg caccgggatg gcttctcctg cagcgatatc	780
gatgagtgcg gctactccag ttacctctgc cagtacc	817

<210> 24

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<212> DNA

<213> Artificial Sequence

<220>

<223> oligonucleotide sens-GAPDH

<400> 24

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<210> 25

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> oligonucleotide antisens-GAPDH

<400> 25

agccttctcc atggtggtga agac	24
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<210> 26

<211> 25
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> oligonucleotide

 <400> 26
 cggttgcct tggggttcag ggggg 25

 <210> 27
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 <220>
 <223> oligonucleotide sens MBP1

 <400> 27
 gccctgatgg ttaccgcaag a 21

 <210> 28
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 <220>
 <223> oligonucleotide antisens MBP1

 <400> 28
 agcccccattg gaagttgaca c 21

 <210> 29
 <211> 20
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 <220>
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 <400> 29
 gtggggcgcc ccaggcacca 20

<210> 30
 <211> 1358
 <212> DNA
 <213> Artificial Sequence
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 <223> Human fragment C-term MBP1: CDS (1)...(885)

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<210> 31
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<212> PRT

<213> Artificial Sequence

<220>

<223> Human fragment C-term MBP1

<400> 31

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35 40 45

Asn Asn Arg Ser Cys Val Asp Val Asn Glu Cys Asp Met Gly Ala Pro
50 55 60

Cys Glu Gln Arg Cys Phe Asn Ser Tyr Gly Thr Phe Leu Cys Arg Cys
65 70 75 80

His Gln Gly Tyr Glu Leu His Arg Asp Gly Phe Ser Cys Ser Asp Ile
85 90 95

Asp Glu Cys Ser Tyr Ser Ser Tyr Leu Cys Gln Tyr Arg Cys Val Asn
100 105 110

Glu Pro Gly Arg Phe Ser Cys His Cys Pro Gln Gly Tyr Gln Leu Leu
115 120 125

Ala Thr Arg Leu Cys Gln Asp Ile Asp Glu Cys Glu Ser Gly Ala His
130 135 140

Gln Cys Ser Glu Ala Gln Thr Cys Val Asn Phe His Gly Gly Tyr Arg
145 150 155 160

Cys Val Asp Thr Asn Arg Cys Val Glu Pro Tyr Ile Gln Val Ser Glu
165 170 175

Asn Arg Cys Leu Cys Pro Ala Ser Asn Pro Leu Cys Arg Glu Gln Pro
180 185 190

Ser Ser Ile Val His Arg Tyr Met Thr Ile Thr Ser Glu Arg Ser Val
195 200 205

Pro Ala Asp Val Phe Gln Ile Gln Ala Thr Ser Val Tyr Pro Gly Ala
210 215 220

Tyr Asn Ala Phe Gln Ile Arg Ala Gly Asn Ser Gln Gly Asp Phe Tyr
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Ile Arg Gln Ile Asn Asn Val Ser Ala Met Leu Val Leu Ala Arg Pro
 245 250 255

Val Thr Gly Pro Arg Glu Tyr Val Leu Asp Leu Glu Met Val Thr Met
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Phe Val Gly Ala Tyr Thr Phe
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 gaaagaaatc attttaaaag gttttttttt ttgctgttgt tgtttaatga taagagtagc 1620
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<210> 33

<211> 333

<212> PRT

<213> Artificial Sequence

<220>

<223> Fragment c-term fibuline 2 murine

<400> 33

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Arg Cys Gly Glu Gly Gln Leu Cys Tyr Asn Leu Pro Gly Ser Tyr Arg
 20 25 30

Cys Asp Cys Lys Pro Gly Phe Gln Arg Asp Ala Phe Gly Arg Thr Cys
 35 40 45

Ile Asp Val Asn Glu Cys Trp Val Ser Pro Gly Arg Leu Cys Gln His
 50 55 60

Thr Cys Glu Asn Thr Pro Gly Ser Tyr Arg Cys Ser Cys Ala Ala Gly
 65 70 75 80

Phe Leu Leu Ala Ala Asp Gly Lys His Cys Glu Asp Val Asn Glu Cys
 Page 20

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Gln	Cys	Tyr	Cys	Arg	Gln	Gly	Tyr	Gln	Leu	Ala	Glu	Asp	Gly	His	Thr		
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Cys	Thr	Asp	Ile	Asp	Glu	Cys	Ala	Gln	Gly	Ala	Gly	Ile	Leu	Cys	Thr		
	130					135					140						
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			260					265					270				
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		275					280					285					
Gly	Val	Val	Ser	Leu	Gln	Arg	Ser	Val	Leu	Glu	Pro	Arg	Asp	Phe	Ala		
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Leu	Asp	Val	Glu	Met	Lys	Leu	Trp	Arg	Gln	Gly	Ser	Val	Thr	Thr	Phe		
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Leu	Ala	Lys	Met	Tyr	Ile	Phe	Phe	Thr	Thr	Phe	Ala	Pro					
				325					330								